

From: Gansheroff, Lisa
Sent: Friday, March 30, 2001 3:02 PM
To: STIC-Biotech/ChemLib
Subject: sequence search 09/582779

Application 09/582779
Please do a sequence search for SEQ ID NO:1.

Thanks!

Lisa Gansheroff
AU 1636
11D03
605-1203

#15
MT
1/29/02

1636

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/582,779ADATE: 03/30/2001
TIME: 15:17:29Input Set : A:\PTO.txt
Output Set : N:\CRF3\03302001\I582779A.raw

ENTERED

3 <110> APPLICANT: Pompejus, Markus
4 Doval, Jose Luis Revuelta
5 Garcia, Maria Angeles Santos
7 <120> TITLE OF INVENTION: Orotidine-5'-phosphate decarboxylase gene, gene construct comprising
8 this gene and its use.

W--> 0 <130> FILE REFERENCE:
10 <140> CURRENT APPLICATION NUMBER: US 09/582,779A
11 <141> CURRENT FILING DATE: 2000-07-03
13 <150> PRIOR APPLICATION NUMBER: Germany/19801120.2
14 <151> PRIOR FILING DATE: 1998-01-15
16 <160> NUMBER OF SEQ ID NOS: 6
18 <170> SOFTWARE: WordPerfect version 6.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 1380
22 <212> TYPE: DNA
23 <213> ORGANISM: Ashbya gossypii
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: 210 ... 1013
29 <400> SEQUENCE: 1

31 ctcgagcaac tcattggaag cccttcgcaa acgacctcta tatctcgtct caagttccta60
33 ctatcatgta tgcgtgcaact acagaaaaat ttttgtctat agctggcaag aagcacatcal20
35 catacattct gatgggtgtag gctccacatc acagtaagca tttgtataag gctgatcacal80
37 taggggtgcta ccgacctagc cattgccac atg tca acg aaa tct tac gca gaa233
38 Met Ser Thr Lys Ser Tyr Ala Glu
39 1 5
41 agg gcc aag gca cac aat tcg cca gtt gct aga aag ctt ctg gca ttg281
42 Arg Ala Lys Ala His Asn Ser Pro Val Ala Arg Lys Leu Leu Ala Leu
43 10 15 20
45 atg cac gag aag aaa acc aat ctc tgc gct tcc ctt gat gtg cgg acg329
46 Met His Glu Lys Lys Thr Asn Leu Cys Ala Ser Leu Asp Val Arg Thr
47 25 30 35 40
49 tct aga aag ctt ctg gag cta gca gac acg ctg gga ccg cac att tgt377
50 Ser Arg Lys Leu Leu Glu Leu Ala Asp Thr Leu Gly Pro His Ile Cys
51 45 50 55
53 ctg ctg aag aca cat gtc gac ata ctg acg gac ttc gac atc gag acg425
54 Leu Leu Lys Thr His Val Asp Ile Leu Thr Asp Phe Asp Ile Glu Thr
55 60 65 70
57 aca gtc aag ccg ctg cag cag ctt gcg gct aag cac aac ttc atg atc473
58 Thr Val Lys Pro Leu Gln Gln Ala Ala Lys His Asn Phe Met Ile
59 75 80 85
61 ttc gag gac cgc aag ttc gct gac att ggc aac acg gtt aag ctg cag521
62 Phe Glu Asp Arg Lys Phe Ala Asp Ile Gly Asn Thr Val Lys Leu Gln
63 90 95 100
65 tac tcc tcc ggc gtg tac cgt atc gcg gag tgg gcg gat att acc aat569
66 Tyr Ser Ser Gly Val Tyr Arg Ile Ala Glu Trp Ala Asp Ile Thr Asn
67 105 110 115 120

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69 gca cac ggc gtc acc ggc ccc ggt gtg ata gcc ggg ctg aag gag gct617
70 Ala His Gly Val Thr Gly Pro Gly Val Ile Ala Gly Leu Lys Glu Ala
71      125      130      135
73 gcg aaa ctg gcc tca cag gaa ccc agg ggg ttg ctg atg ctg gca gag665
74 Ala Lys Leu Ala Ser Gln Glu Pro Arg Gly Leu Leu Met Leu Ala Glu
75      140      145      150
77 ctc tct tct cag ggc tct ttg gcg cgc gga gac tat acc gcg ggc gtc713
78 Leu Ser Ser Gln Gly Ser Leu Ala Arg Gly Asp Tyr Thr Ala Gly Val
79      155      160      165
81 gtt gaa atg gcg aag ctg gac gaa gac ttt gtg atc ggg ttc atc gcg761
82 Val Glu Met Ala Lys Leu Asp Glu Asp Phe Val Ile Gly Phe Ile Ala
83      170      175      180
85 cag cgt gac atg ggt ggg cgt gca gac ggc ttt gac tgg ctc atc atg809
86 Gln Arg Asp Met Gly Gly Arg Ala Asp Gly Phe Asp Trp Leu Ile Met
87 185      190      195      200
89 acc ccg ggg gtt ggc ctg gac gac aaa gga gac ggc ctg ggc cag cag857
90 Thr Pro Gly Val Gly Leu Asp Asp Lys Gly Asp Gly Leu Gly Gln Gln
91      205      210      215
93 tac cgc acg gtg gat gag gtc gtc agc gac ggt acc gat gtg atc att905
94 Tyr Arg Thr Val Asp Glu Val Val Ser Asp Gly Thr Asp Val Ile Ile
95      220      225      230
97 gtt ggc aga ggg ctc ttt gac aag gga aga gac ccc aag gtc gag ggt953
98 Val Gly Arg Gly Leu Phe Asp Lys Gly Arg Asp Pro Lys Val Glu Gly
99      235      240      245
101 gcc cgc tac cgc aag gcc ggt tgg gag gct tac ttg cgc cgt atg ggc1001
102 Ala Arg Tyr Arg Lys Ala Gly Trp Glu Ala Tyr Leu Arg Arg Met Gly
103      250      255      260
105 gag act tcg tagtctatcg ctggcgccca cagtatatag gcggattcca      1050
106 Glu Thr Ser
107 265
109 ccgcgatta ccattctcagc aacctttttg taattatatg cccctattgc ccttatttcc1110
111 gagctggtgc cgggatcggg ttatagacgg gcaacaagtt gatactttgt tcagtagcat1170
113 gcatccaaca cttgcaggct tggggtgtgg aaggcctcgc cgcggataat tcgtattacc1230
115 cgcacttcgt gaagtattgc tttatgaaaa atcttcactt tgggctaact agagccataa1290
117 ctcgacacaa gcccttcct acacacttcg agctgggact aaagtgacaa cgaatagcaa1350
119 ataattagca aatatggatg cgttgaattc      1380
122 <210> SEQ ID NO: 2
123 <211> LENGTH: 267
124 <212> TYPE: PRT
125 <213> ORGANISM: Ashbya gossypii
127 <400> SEQUENCE: 2
129 Met Ser Thr Lys Ser Tyr Ala Glu Arg Ala Lys Ala His Asn Ser Pro
130 1      5      10      15
132 Val Ala Arg Lys Leu Leu Ala Leu Met His Glu Lys Lys Thr Asn Leu
133      20      25      30
135 Cys Ala Ser Leu Asp Val Arg Thr Ser Arg Lys Leu Leu Glu Leu Ala
136      35      40      45
138 Asp Thr Leu Gly Pro His Ile Cys Leu Leu Lys Thr His Val Asp Ile
139      50      55      60

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```

141 Leu Thr Asp Phe Asp Ile Glu Thr Thr Val Lys Pro Leu Gln Gln Leu
142 65 70 75 80
144 Ala Ala Lys His Asn Phe Met Ile Phe Glu Asp Arg Lys Phe Ala Asp
145 85 90 95
147 Ile Gly Asn Thr Val Lys Leu Gln Tyr Ser Ser Gly Val Tyr Arg Ile
148 100 105 110
150 Ala Glu Trp Ala Asp Ile Thr Asn Ala His Gly Val Thr Gly Pro Gly
151 115 120 125
153 Val Ile Ala Gly Leu Lys Glu Ala Ala Lys Leu Ala Ser Gln Glu Pro
154 130 135 140
156 Arg Gly Leu Leu Met Leu Ala Glu Leu Ser Ser Gln Gly Ser Leu Ala
157 145 150 155 160
159 Arg Gly Asp Tyr Thr Ala Gly Val Val Glu Met Ala Lys Leu Asp Glu
160 165 170 175
162 Asp Phe Val Ile Gly Phe Ile Ala Gln Arg Asp Met Gly Gly Arg Ala
163 180 185 190
165 Asp Gly Phe Asp Trp Leu Ile Met Thr Pro Gly Val Gly Leu Asp Asp
166 195 200 205
168 Lys Gly Asp Gly Leu Gly Gln Gln Tyr Arg Thr Val Asp Glu Val Val
169 210 215 220
171 Ser Asp Gly Thr Asp Val Ile Ile Val Gly Arg Gly Leu Phe Asp Lys
172 225 230 235 240
174 Gly Arg Asp Pro Lys Val Glu Gly Ala Arg Tyr Arg Lys Ala Gly Trp
175 245 250 255
177 Glu Ala Tyr Leu Arg Arg Met Gly Glu Thr Ser
178 260 265

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180 <210> SEQ ID NO: 3

181 <211> LENGTH: 18

182 <212> TYPE: DNA

183 <213> ORGANISM: Unknown

185 <220> FEATURE:

186 <221> NAME/KEY: misc_feature

187 <222> LOCATION: 1 ... 18

188 <223> OTHER INFORMATION: n represents g, a, t or c

W--> 189 <220> FEATURE:

190 <223> OTHER INFORMATION: oligonucleotide as primer for PCR

192 <400> SEQUENCE: 3

W--> 194 ytnngnccnt ayathtgy

197 <210> SEQ ID NO: 4

198 <211> LENGTH: 23

199 <212> TYPE: DNA

200 <213> ORGANISM: Unknown

202 <220> FEATURE:

203 <221> NAME/KEY: misc_feature

204 <222> LOCATION: 1 ... 23

205 <223> OTHER INFORMATION: n represents g, a, t or c

W--> 206 <220> FEATURE:

207 <223> OTHER INFORMATION: oligonucleotide as primer for PCR

209 <400> SEQUENCE: 4

18

RAW SEQUENCE LISTING
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Input Set : A:\PTO.txt
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OK 211 taytgytgnc cnaryttrtc ncc 23
214 <210> SEQ ID NO: 5
215 <211> LENGTH: 26
216 <212> TYPE: DNA
217 <213> ORGANISM: Unknown
219 <220> FEATURE:
220 <221> NAME/KEY: misc_feature
221 <222> LOCATION: 1 ... 26
222 <223> OTHER INFORMATION: n represents g, a, t or c
Wf-> 223 <220> FEATURE:
224 <223> OTHER INFORMATION: oligonucleotide as primer for PCR
226 <400> SEQUENCE: 5
Wf-> 228 ttyytnatht tygargaymg naartt 26
231 <210> SEQ ID NO: 6
232 <211> LENGTH: 19
233 <212> TYPE: DNA
234 <213> ORGANISM: Unknown
236 <220> FEATURE:
237 <221> NAME/KEY: misc_feature
238 <222> LOCATION: 1 ... 19
239 <223> OTHER INFORMATION: n represents g, a, t or c
Wf-> 240 <220> FEATURE:
241 <223> OTHER INFORMATION: oligonucleotide as primer for PCR
243 <400> SEQUENCE: 6
Wf-> 245 gcnarnarna rnarnccnc 19

VERIFICATION SUMMARY

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L:0 M:201 W: Mandatory field data missing, FILE REFERENCE
L:189 M:283 W: Missing Blank Line separator, <220> field identifier
L:194 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:206 M:283 W: Missing Blank Line separator, <220> field identifier
L:211 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:223 M:283 W: Missing Blank Line separator, <220> field identifier
L:228 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:240 M:283 W: Missing Blank Line separator, <220> field identifier
L:245 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6